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AMENDMENTS TO THE CLAIMS

Claims 1-24 (canceled)

- 25. (previously presented) An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2.
- 26. (previously presented) A composition comprising the isolated polypeptide of claim 25 and an acceptable carrier.
- 27. (previously presented) The isolated polypeptide of claim 25, wherein the isolated polypeptide comprises a heterologous amino acid sequence fused to the amino acid sequence set forth in SEQ ID NO: 2.
- 28. (previously presented) A composition comprising the isolated polypeptide of claim 27 and an acceptable carrier.
- 29. (previously presented) The isolated polypeptide of claim 25, wherein the isolated polypeptide consists of the amino acid sequence set forth in SEQ ID NO: 2.
- 30. (previously presented) A composition comprising the isolated polypeptide of claim 29 and an acceptable carrier.
- 31. (currently amended) An isolated polypeptide fragment comprising at least 50 consecutive amino acids of SEQ ID NO: 2 wherein said polypeptide fragment comprises the amino acid at position 191 of SEQ ID NO: 2, wherein said amino acid is glycine or a conservative substitution thereof, and wherein the polypeptide fragment comprises at least one biological activity of Fab I is capable of reducing crotonyl-CoA or crotonyl-ACP.
- 32. (previously presented) The isolated polypeptide fragment of claim 31, wherein the isolated polypeptide fragment comprises a heterologous amino acid sequence fused to the at least 50 consecutive amino acids of SEQ ID NO: 2.
- 33. (currently amended) An isolated polypeptide fragment comprising at least 30 consecutive amino acids of SEQ ID NO: 2 wherein said polypeptide fragment comprises the amino acid at position 191 of SEQ ID NO: 2, wherein said amino acid is glycine or a conservative substitution thereof, and wherein the polypeptide fragment comprises at least one biological activity of Fab I is capable of reducing crotonyl-CoA or crotonyl-ACP.

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- 34. (previously presented) The isolated polypeptide fragment of claim 35, wherein the isolated polypeptide fragment comprises a heterologous amino acid sequence fused to the at least 30 consecutive amino acids of SEQ ID NO: 2.
- 35. (currently amended) An isolated polypeptide, wherein said polypeptide comprises an amino acid sequence encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of a polynucleotide having at least 95% identity with the polynucleotide sequence set forth in SEQ ID NO: 1-and wherein said polypeptide comprises the amino acid at position 191 of SEQ ID NO: 2, or its equivalent, and said amino acid is glycine or a conservative substitution thereof.
- 36. (currently amended) An isolated polypeptide comprising an amino acid sequence having at least 95% identity with the amino acid sequence set forth in SEQ ID NO: 2, wherein said polypeptide comprises the amino acid at position 191 of SEQ ID NO: 2, or its equivalent, and said amino acid is glycine or a conservative substitution thereof.
- 37. (currently amended) An isolated polypeptide, comprising an amino acid sequence comprising SEQ ID NO: 2 with 0 to 10 conservative amino acid substitutions, wherein said polypeptide comprises the amino acid at position 191 of SEQ ID NO: 2, or its equivalent, and said amino acid is glycine or a conservative substitution thereof.